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1652

RAW SEQUENCE LISTING

DATE: 07/10/2002

PATENT APPLICATION: US/09/358,103C

TIME: 15:42:18

Input Set : A:\Reca.app

Output Set: N:\CRF3\07102002\I358103C.raw

P.6

3 <110> APPLICANT: Roca, Alberto I
 5 <120> TITLE OF INVENTION: Mutants of Maw Motifs of RecA Protein Homologs, Methods
 6 of Making Them, and Their Uses
 8 <130> FILE REFERENCE: RecA Homolog Protein & Mutants
 10 <140> CURRENT APPLICATION NUMBER: 09/358,103C
 11 <141> CURRENT FILING DATE: 1999-07-21
 13 <150> PRIOR APPLICATION NUMBER: 60/094,071
 14 <151> PRIOR FILING DATE: 1998-07-24
 16 <160> NUMBER OF SEQ ID NOS: 3
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 26
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Escherichia coli
 25 <220> FEATURE:
 26 <221> NAME/KEY: NON_TER
 27 <222> LOCATION: (1)
 29 <220> FEATURE:
 30 <221> NAME/KEY: NON_TER
 31 <222> LOCATION: (26)..)
 33 <220> FEATURE:
 34 <221> NAME/KEY: HELIX
 35 <222> LOCATION: (6)..(12)
 36 <223> OTHER INFORMATION: Alpha-helix B
 38 <220> FEATURE:
 39 <221> NAME/KEY: STRAND
 40 <222> LOCATION: (22)..(26)
 41 <223> OTHER INFORMATION: Beta-strand 1
 43 <220> FEATURE:
 44 <221> NAME/KEY: SIMILAR
 45 <222> LOCATION: (1)..(26)
 46 <223> OTHER INFORMATION: This structure is highly conserved across
 47 bacterial RecA and homologous eukaryotic,
 48 archaeal, and viral proteins; sequence below is
 49 from E. coli RecA positions 40-65
 51 <400> SEQUENCE: 1
 52 Ile Ser Thr Gly Ser Leu Ser Leu Asp Ile Ala Leu Gly Ala Gly Gly
 53 1 5 10 15
 55 Leu Pro Met Gly Arg Ile Val Glu Ile Tyr
 56 20 25
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 26
 61 <212> TYPE: PRT

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62 <213> ORGANISM: Escherichia coli
64 <220> FEATURE:
65 <221> NAME/KEY: NON_TER
66 <222> LOCATION: (1)
68 <220> FEATURE:
69 <221> NAME/KEY: NON_TER
70 <222> LOCATION: (26)
72 <220> FEATURE:
73 <221> NAME/KEY: HELIX
74 <222> LOCATION: (6)..(12)
75 <223> OTHER INFORMATION: Alpha-helix B
77 <220> FEATURE:
78 <221> NAME/KEY: STRAND
79 <222> LOCATION: (22)..(26)
80 <223> OTHER INFORMATION: Beta-strand 1
82 <220> FEATURE:
83 <221> NAME/KEY: SIMILAR
84 <222> LOCATION: (1)..(26)
85 <223> OTHER INFORMATION: Non 'Xaa' residues are the invariant MAW-motif
86 residues in RecA and its homologs
88 <220> FEATURE:
89 <221> NAME/KEY: SITE
90 <222> LOCATION: (1)
91 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
92 and has been observed to contain Ile, Phe, Met, Thr,
93 Val, Tyr, or Leu
95 <220> FEATURE:
96 <221> NAME/KEY: SITE
97 <222> LOCATION: (2)
98 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
99 and has been observed to contain Ser, Gly, Lys,
100 Pro, Thr, or Arg
102 <220> FEATURE:
103 <221> NAME/KEY: SITE
104 <222> LOCATION: (3)
105 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
106 and has been observed to contain Thr, Ser, or Trp
108 <220> FEATURE:
109 <221> NAME/KEY: SITE
110 <222> LOCATION: (4)
111 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
112 and has been observed to contain Gly, Arg, Ala,
113 Lys, Asn, or Gln
115 <220> FEATURE:
116 <221> NAME/KEY: SITE
117 <222> LOCATION: (5)
118 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
119 and has been observed to contain Ser, Ala, Cys,
120 Ile, Asn, Asp, or Phe

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122 <220> FEATURE:
123 <221> NAME/KEY: SITE
124 <222> LOCATION: (6)
125 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
126 and has been observed to contain Leu, Ile, Thr,
127 Val, Tyr, Lys, Gln, Asp, Pro, or Arg
129 <220> FEATURE:
130 <221> NAME/KEY: SITE
131 <222> LOCATION: (7)
132 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
133 and has been observed to contain Ser, Ala, Asp,
134 Gly, Leu, Met, Thr, Val, Tyr, Glu, Asn, or Gln
136 <220> FEATURE:
137 <221> NAME/KEY: SITE
138 <222> LOCATION: (8)
139 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
140 and has been observed to contain Leu, Ile, Val,
141 Phe, or Met
143 <220> FEATURE:
144 <221> NAME/KEY: SITE
145 <222> LOCATION: (9)
146 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
147 and has been observed to contain Asp or Asn
149 <220> FEATURE:
150 <221> NAME/KEY: SITE
151 <222> LOCATION: (10)
152 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
153 and has been observed to contain Ile, Ala, Glu,
154 Gly, Leu, Asn, Gln, Arg, Ser, Thr, Val, Lys, or
155 Asp
157 <220> FEATURE:
158 <221> NAME/KEY: SITE
159 <222> LOCATION: (11)
160 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
161 and has been observed to contain Ala, Ile, Leu, or
162 Val
164 <220> FEATURE:
165 <221> NAME/KEY: SITE
166 <222> LOCATION: (12)
167 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
168 and has been observed to contain Leu, Met, or Thr
170 <220> FEATURE:
171 <221> NAME/KEY: SITE
172 <222> LOCATION: (13)
173 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
174 and has been observed to contain Gly, Gln, Ala,
175 Asn, or Ser
177 <220> FEATURE:
178 <221> NAME/KEY: SITE

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179 <222> LOCATION: (14)
180 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
181 and has been observed to contain Ala, Ile, Ser,
182 Thr, Val, Gly, or Leu, and this site is not
183 present in some homologs
185 <220> FEATURE:
186 <221> NAME/KEY: SITE
187 <222> LOCATION: (17)
188 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
189 and has been observed to contain Leu, Phe, Ile,
190 Val, Tyr, or Met
192 <220> FEATURE:
193 <221> NAME/KEY: SITE
194 <222> LOCATION: (18)
195 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
196 and has been observed to contain Pro, Glu, Met,
197 Phe, Gln, Arg, or Val
199 <220> FEATURE:
200 <221> NAME/KEY: SITE
201 <222> LOCATION: (19)
202 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
203 and has been observed to contain Met, Gly, Lys,
204 Arg, Thr, Ala, Pro, or Ser
206 <220> FEATURE:
207 <221> NAME/KEY: SITE
208 <222> LOCATION: (20)
209 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
210 and has been observed to contain Gly, Leu, Met,
211 Ala, His, Gln, or Arg
213 <220> FEATURE:
214 <221> NAME/KEY: SITE
215 <222> LOCATION: (21)
216 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
217 and has been observed to contain Arg, Gln, Ser,
218 Gly, Thr, or Val
220 <220> FEATURE:
221 <221> NAME/KEY: SITE
222 <222> LOCATION: (22)
223 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
224 and has been observed to contain Ile, Val, Ala,
225 Leu, or Met
227 <220> FEATURE:
228 <221> NAME/KEY: SITE
229 <222> LOCATION: (23)
230 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
231 and has been observed to contain Val, Ile, Thr, or
232 Tyr
234 <220> FEATURE:
235 <221> NAME/KEY: SITE

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236 <222> LOCATION: (25)
237 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
238     and has been observed to contain Ile, Val, Ala,
239     Leu, Met, or Phe
241 <220> FEATURE:
242 <221> NAME/KEY: SITE
243 <222> LOCATION: (26)
244 <223> OTHER INFORMATION: This site is not invariant across RecA homologs
245     and has been observed to contain Tyr, Phe, Ala,
246     Gly, or Val
248 <400> SEQUENCE: 2
W--> 249 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Gly
      250   1               5               10               15
W--> 252 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa
      253           20           25
256 <210> SEQ ID NO: 3
257 <211> LENGTH: 26
258 <212> TYPE: PRT
259 <213> ORGANISM: Escherichia coli
261 <220> FEATURE:
262 <221> NAME/KEY: NON_TER
263 <222> LOCATION: (1)
265 <220> FEATURE:
266 <221> NAME/KEY: NON_TER
267 <222> LOCATION: (26)
269 <220> FEATURE:
270 <221> NAME/KEY: HELIX
271 <222> LOCATION: (6)..(12)
272 <223> OTHER INFORMATION: Alpha-helix B
274 <220> FEATURE:
275 <221> NAME/KEY: STRAND
276 <222> LOCATION: (22)..(26)
277 <223> OTHER INFORMATION: Beta-strand 1
279 <220> FEATURE:
280 <221> NAME/KEY: SIMILAR
281 <222> LOCATION: (1)..(26)
282 <223> OTHER INFORMATION: Non "Xaa" residues are the invariant and
283     semiconservative elements of the MAW motif in RecA
284     and its homologs
286 <220> FEATURE:
287 <221> NAME/KEY: SITE
288 <222> LOCATION: (2)
289 <223> OTHER INFORMATION: This site is neither invariant nor
290     semiconservative across RecA homologs and has been
291     observed to contain Ser, Gly, Lys, Pro, Thr, or
292     Arg
294 <220> FEATURE:
295 <221> NAME/KEY: SITE
296 <222> LOCATION: (5)

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RAW SEQUENCE LISTING ERROR SUMMARY
 PATENT APPLICATION: US/09/358,103C

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,17,18,19,20,21,22,23,25
 Seq#:2; Xaa Pos. 26
 Seq#:3; Xaa Pos. 2,5,6,7,10,13,14,18,19,21

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
 Seq#:1; Line(s) 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
 Seq#:1; Line(s) 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59
 Seq#:2; Line(s) 60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79
 Seq#:2; Line(s) 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99
 Seq#:2; Line(s) 100,101,102,103,104,105,106,107,108,109,110,111,112,113,114
 Seq#:2; Line(s) 115,116,117,118,119,120,121,122,123,124,125,126,127,128,129
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 Seq#:2; Line(s) 190,191,192,193,194,195,196,197,198,199,200,201,202,203,204
 Seq#:2; Line(s) 205,206,207,208,209,210,211,212,213,214,215,216,217,218,219
 Seq#:2; Line(s) 220,221,222,223,224,225,226,227,228,229,230,231,232,233,234
 Seq#:2; Line(s) 235,236,237,238,239,240,241,242,243,244,245,246,247,248,249
 Seq#:2; Line(s) 250,251,252,253,254,255,256
 Seq#:3; Line(s) 257,258,259,260,261,262,263,264,265,266,267,268,269,270,271
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